IN THE CLAIMS:

Applicants, pursuant to 37 CFR § 1.121, submit the following amendment to the Claims:

By this Response, no claim amendments are made.

1. (Previously presented) A method for detecting and/or for detecting and distinguishing between or among colon cell proliferative disorders in a subject comprising:

a) contacting genomic DNA isolated from blood plasma, blood serum, whole blood, isolated blood cells, or cells isolated from the blood obtained from a subject with at least one reagent, or series of reagents that distinguishes between methylated and non-methylated CpG dinucleotides within at least one target region of the genomic DNA, wherein said contiguous nucleotides comprise at least one CpG dinucleotide sequence; and

b) detecting, or detecting and distinguishing between or among colon cell proliferative disorders, wherein the detecting, or detecting and distinguishing is with a sensitivity of greater than or equal to 80% and a specificity of greater than or equal to 80%.

2. (Previously presented) The method of claim 1, wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of the ALX 4 gene sequence.

3. (Previously presented) A method for detecting, or for detecting and distinguishing between or among colon cell proliferative disorders in a subject, comprising determining, in a biological sample isolated from a subject, the expression levels of the ALX 4 gene or gene sequences thereof.

4. (Previously presented) The method of claim 3, wherein said expression level is determined by detecting the presence, absence or level of mRNA transcribed from said gene or sequence.

5. (Previously presented) The method of claim 3, wherein said expression level is determined by detecting the presence, absence or level of a polypeptide encoded by said gene or

sequence.

6. (Previously presented) The method of claim 5, wherein said polypeptide is detected by one or more means selected from the group consisting of immunoassay, ELISA immunoassay, radioimmunoassay and antibody.

7. (Previously presented) The method of claim 3, wherein said expression is determined by detecting the presence or absence of CpG methylation within said gene or sequence, wherein hypermethylation indicates the presence of a colon cell proliferative disorder.

8. (Previously presented) A method for detecting, or for detecting and distinguishing between or among colon cell proliferative disorders in a subject, comprising contacting genomic DNA isolated from a biological sample obtained from a subject with at least one reagent, or series of reagents that distinguishes between methylated and non-methylated CpG dinucleotides within at least one target region of the genomic DNA, wherein the at least one target region comprises, or hybridizes under stringent conditions to a sequence of at least 16 contiguous nucleotides of the ALX 4 gene sequence, wherein said contiguous nucleotides comprise at least one CpG dinucleotide sequence, and whereby detecting, or detecting and distinguishing between or among colon cell proliferative disorders is afforded.

9. (Cancelled)

10. (Previously presented) The method of claim 8, wherein colorectal carcinoma is distinguished from at least one condition selected from the group consisting of colon adenoma, normal colon tissue, non-colon tissues and non-colon cell proliferative disorders.

11. (Previously presented) The method of claim 8, wherein colon adenoma is distinguished from at least one condition selected from the group consisting of colon carcinoma, normal colon tissue, non-colon tissues and non-colon cell proliferative disorders.

12. (Previously presented) The method of claim 8, wherein at least one of colorectal carcinoma tissue or colon adenomas is distinguished from at least one tissue selected from the group consisting of colon polyps less than 1cm in diameter, inflammatory colon tissue, and normal colon tissue, and wherein the target region comprises, or hybridizes under stringent conditions to

at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:5, and complements thereof.

13. (Previously presented) The method of claim 8, wherein colorectal carcinoma is distinguished from at least one tissue selected from the group consisting of non-colon healthy tissue, peripheral blood lymphocytes and non-colon cancer tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:5, and complements thereof.

14. (Previously presented) The method of claim 8, wherein colorectal carcinoma is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue, normal colon tissue, non-colon healthy tissue, peripheral blood lymphocytes, colon adenomas and non-colon cancer tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:5, and complements thereof.

15. (Previously presented) The method of claim 8, wherein colorectal carcinoma is distinguished from colon adenomas, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:5, and complements thereof.

16. (Previously presented) The method of claim 8, wherein at least one of colorectal carcinoma tissue, or large adenomas is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue, and normal colon tissue.

17. (Previously presented) The method of claim 8, wherein colorectal carcinoma tissue is distinguished from at least one of inflammatory colon tissue and normal colon tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:5, and complements thereof.

18. (Previously presented) The method of claim 1, wherein at least one of colorectal carcinoma tissue, or colon adenomas is distinguished from at least one tissue selected from the

group consisting of inflammatory colon tissue, normal colon tissue, non-colon healthy tissue, peripheral blood lymphocytes, and non-colon cancer tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:5, and complements thereof.

19. (Previously presented) The method of claim 8, wherein tissues originating from the colon are distinguished from tissues of non-colon origin.

20. (Previously presented) A method for detecting, or for detecting and distinguishing between or among cell proliferative disorders and healthy tissues in a subject, comprising contacting genomic DNA isolated from a biological sample obtained from a subject with at least one reagent, or series of reagents that distinguishes between methylated and non-methylated CpG dinucleotides within at least one target region of the genomic DNA, wherein the at least one target region comprises, or hybridizes under stringent conditions to a sequence of at least 16 contiguous nucleotides of at least two sequences selected from the group consisting of SEQ ID NOS:5 and complements thereof, wherein said contiguous nucleotides comprise at least one CpG dinucleotide sequence.

21. (Previously presented) The method of claim 8, comprising:

a) extracting or otherwise isolating genomic DNA from a biological sample obtained from a subject;

b) treating the genomic DNA, or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties;

c) contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence of at least 9 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429SEQ ID NOS:304 to SEQ ID NO:535 and SEQ ID NOS:65 to SEQ ID NO:88, and complements thereof, wherein the treated genomic DNA or the fragment thereof is either

amplified to produce at least one amplificate, or is not amplified; and

d) determining, based on a presence or absence of, or on a property of said amplificate, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of SEQ ID NOS:5, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotides of a sequence selected from the groups consisting of SEQ ID NOS:5, whereby at least one of detecting, or detecting and distinguishing between colon cell proliferative disorders is, at least in part, afforded.

22. (Previously presented) The method of claim 21, wherein treating the genomic DNA, or the fragment thereof, comprises use of at least one reagent selected from the group consisting of bisulfite, hydrogen sulfite, and disulfite.

23. (Previously presented) The method of claim 21, wherein contacting or amplifying in c) comprises use of at least one method selected from the group consisting of: use of a heat-resistant DNA polymerase as the amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); and generation of a amplificate nucleic acid molecule carrying a detectable label.

24. (Original) The method of claim 23, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.

25. (Original) The method of claim 21, wherein the biological sample obtained from the subject is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, stool, colonic effluent, urine, blood plasma, blood serum, whole blood, isolated blood cells, cells isolated from the blood and combinations thereof.

26. (Previously presented) The method of claim 21, further comprising in step d) the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case

a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized.

27. (Previously presented) The method of claim 26, wherein the sequence of said nucleic acid molecules is selected from the group consisting of SEQ ID NOS: 3030, 3035, 3046, 3058, 3062, 3067, 3070, 3074, 3077, 3079, 3082, 3087, 3095, 3099, 3102, 3106, 3112, 3120, 3125, 3129, 3132, 3141, 3143, 3154, 3156, and 3158.

28. (Original) The method of claim 26, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case modified at the 5'-end thereof to preclude degradation by an enzyme having 5'-3' exonuclease activity.

29. (Original) The method of claim 26, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case lacking a 3' hydroxyl group.

30. (Original) The method of claim 26, wherein the amplification enzyme is a polymerase lacking 5'-3' exonuclease activity.

31. (Previously presented) The method of claim 21, wherein determining in d) comprises hybridization of at least one nucleic acid molecule or peptide nucleic acid molecule in each case comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof.

32. (Previously presented) The method of claim 31, wherein said nucleic acid is taken from the group consisting of SEQ ID NOS:3030, 3035, 3046, 3058, 3062, 3067, 3070, 3074, 3077, 3079, 3082, 3087, 3095, 3099, 3102, 3106, 3112, 3120, 3125, 3129, 3132, 3141, 3143, 3154, 3156, and 3158.

33. (Original) The method of claim 31, wherein at least one such hybridizing nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase.

34. (Original) The method of claim 31, wherein a plurality of such hybridizing nucleic acid molecules or peptide nucleic acid molecules are bound to a solid phase in the form of a nucleic acid or peptide nucleic acid array selected from the array group consisting of linear or substantially so, hexagonal or substantially so, rectangular or substantially so, and combinations thereof.

35. (Original) The method of claim 31, further comprising extending at least one such hybridized nucleic acid molecule by at least one nucleotide base.

36. (Previously presented) The method of claim 21, wherein determining in d), comprises sequencing of the amplificate.

37. (Original) The method of claim 21, wherein contacting or amplifying in c), comprises use of methylation-specific primers.

38. (Previously presented) The method of claim 37, wherein the sequence of said methylation-specific primers is selected from the group consisting of SEQ ID NOS:3028, 3032, 3033, 3036, 3037, 3038, 3039, 3041, 3042, 3043, 3044, 3047, 3048, 3049, 3052, 3055, 3059, 3061, 3064, 3065, 3068, 3069, 3071, 3072, 3075, 3076, 3080, 3083, 3084, 3085, 3086, 3091, 3093, 3096, 3097, 3100, 3104, 3109, 3110, 3113, 3115, 3117, 3118, 3123, 3126, 3127, 3130, 3134, 3135, 3136, 3138, 3139, 3144, 3146, 3147, 3149, 3150, 3155, 3029, 3031, 3034, 3040, 3045, 3050, 3051, 3053, 3054, 3056, 3057, 3060, 3063, 3066, 3073, 3078, 3081, 3088, 3089, 3090, 3092, 3094, 3098, 3101, 3103, 3105, 3107, 3108, 3111, 3114, 3116, 3119, 3121, 3122, 3124, 3128, 3131, 3133, 3137, 3140, 3142, 3145, 3148, 3151, 3152, 3153, and 3157.

39. (Previously presented) The method of claim 21, comprising in c) using primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides; and further comprising in d) the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a

solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing in d) of the amplificate.

40. (Previously presented) The method of claim 21, comprising in c) use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized; and further comprising in d) the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing in d) of the amplificate.

41. (Previously presented) The method of claim 21, comprising in c) amplification by primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides and further comprising in d) hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429.

42. (Previously presented) The method of claim 21, comprising in c) the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized, and further comprising in d) hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under ~~moderately stringent or~~ stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and complements thereof.

43. (Previously presented) The method of claim 39, wherein the primer oligonucleotides of c) are selected from the group consisting SEQ ID NOS: 3028, 3032, 3033, 3036, 3037, 3038, 3039, 3041, 3042, 3043, 3044, 3047, 3048, 3049, 3052, 3055, 3059, 3061, 3064, 3065, 3068, 3069, 3071, 3072, 3075, 3076, 3080, 3083, 3084, 3085, 3086, 3091, 3093, 3096, 3097, 3100, 3104, 3109, 3110, 3113, 3115, 3117, 3118, 3123, 3126, 3127, 3130, 3134, 3135, 3136, 3138, 3139, 3144, 3146, 3147, 3149, 3150, 3155, 3029, 3031, 3034, 3040, 3045, 3050, 3051, 3053, 3054, 3056, 3057, 3060, 3063, 3066, 3073, 3078, 3081, 3088, 3089, 3090, 3092, 3094, 3098, 3101, 3103, 3105, 3107, 3108, 3111, 3114, 3116, 3119, 3121, 3122, 3124, 3128, 3131, 3133, 3137, 3140, 3142, 3145, 3148, 3151, 3152, 3153, and 3157.

44. (Cancelled)

45. (Previously presented) A method for detecting, or for detecting and distinguishing

between or among colon cell proliferative disorders in a subject, comprising:

a) obtaining, from a subject, a biological sample having subject genomic DNA;

b) extracting, or otherwise isolating the genomic DNA;

c) contacting the genomic DNA of b), or a fragment thereof, comprising at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NO:5 and sequences that hybridize under stringent conditions thereto, with one or more methylation-sensitive restriction enzymes, wherein the genomic DNA is, with respect to each cleavage recognition motif thereof, either cleaved thereby to produce cleavage fragments, or not cleaved thereby; and

d) determining, based on a presence or absence of, or on property of at least one such cleavage fragment, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of SEQ ID NO:5, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotides of a sequence selected from the group consisting of SEQ ID NO:5, whereby at least one of detecting, or of detecting and differentiating between or among colon cell proliferative disorders is~~, at least in part,~~ afforded.

46. (Withdrawn) A treated nucleic acid derived from genomic SEQ ID NOS:5, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.

47. (Withdrawn) A nucleic acid, comprising at least 16 contiguous nucleotides of a treated genomic DNA sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429, and sequences complementary thereto, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.

48. (Withdrawn) The nucleic acid of claim 46, wherein the contiguous base sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.

49. (Withdrawn) The nucleic acid of claim 46, wherein the treatment comprises use of

a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof.

50. (Withdrawn) An oligomer, comprising a sequence of at least 9 contiguous nucleotides that is complementary to, or hybridizes under stringent conditions to a treated genomic DNA sequence selected from the group consisting of SEQ ID NOS:312, 313, 428 and 429.

51. (Withdrawn) The oligomer of Claim 49, comprising at least one CpG , CpA or TpG dinucleotide sequence.

52. (Cancelled)

53. (Withdrawn) A kit useful for detecting, or for detecting and differentiating between or among colon cell proliferative disorders of a subject, comprising:

-a methylation-sensitive restriction enzyme; and

-at least one nucleic acid molecule or peptide nucleic acid molecule, comprising a contiguous sequence of at least 16 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:5, and complements thereof.

54. (Cancelled)

55. (Withdrawn) A kit useful for detecting, or for detecting and differentiating between or among colon cell proliferative disorders of a subject, comprising:

-a bisulfite reagent; and

-at least one nucleic acid molecule or peptide nucleic acid molecule, comprising a contiguous sequence of at least 16 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:312, 312, 428 and 429, and complements thereof.

56. (Cancelled)

57. (Withdrawn) The kit of claim 54, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethyLight, HeavyMethyl, COBRA, nucleic acid sequencing, and combinations thereof.

58. (Withdrawn) The kit of claim 52, wherein the length of the contiguous nucleotide sequence is selected from the group consisting of at least 17, at least 18, at least 20, at least 22, at least 23, at least 25, at least 27, at least 30, and at least 35 nucleotides.

59. (Withdrawn) The kit of claim 52, wherein the length of the contiguous nucleotide sequence is at least 18 nucleotides.